STIC Biotechnology Systems Branch

RAW SEQUENCE LISTING
ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: *10/560,269*
Source: *1FWP*
Date Processed by STIC: *12/20/05*

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:
1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY
FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT
MARK SPENCER, TELEPHONE: 571-272-2510; FAX: 571-273-0221

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE <u>CHECKER VERSION 4.2.2 PROGRAM</u>, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:
   http://www.uspto.gov/web/offices/pac/checker/chkrnote.htm

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.
Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.
Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<http://www.uspto.gov/ebc/efs/downloads/documents.htm> , EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. Hand Carry, Federal Express, United Parcel Service, or other delivery service (EFFECTIVE 01/14/05): U.S. Patent and Trademark Office, Mail Stop Sequence, Customer Window, Randolph Building, 401 Dulany Street, Alexandria, VA 22314

Revised 01/24/05

Raw Sequence Listing Error Summary

ERROR DETECTED   **SUGGESTED CORRECTION**   SERIAL NUMBER: _10/560,269_

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

1_____Wrapped Nucleics   The number/text at the end of each line "wrapped" down to the next line. This may occur if your file
    Wrapped Aminos   was retrieved in a word processor **after** creating it. Please adjust your right margin to .3; this will
     prevent "wrapping."

2_____Invalid Line Length   The rules require that a line **not exceed 72 characters** in length. This includes white spaces.

3_____Misaligned Amino   The numbering under each 5th amino acid is misaligned. Do **not** use tab codes between numbers;
    Numbering   use **space characters**, instead.

4_____Non-ASCII   The submitted file was **not** saved in ASCII(DOS) text, as **required** by the Sequence Rules. **Please
     ensure your subsequent submission is saved in ASCII text.**

5_√_Variable Length   Sequence(s) ___ contain n's or Xaa's representing more than one residue. **Per Sequence Rules,
     each n or Xaa can only represent a single residue.** Please present the **maximum** number of each
     residue having variable length and indicate in the <220>-<223> section that some may be missing.

6_____PatentIn 2.0   A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid
    "bug"   sequences(s) _____. Normally, PatentIn would automatically generate this section from the
     previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to
     the subsequent amino acid sequence. **This applies to the mandatory <220>-<223> sections for
     Artificial or Unknown sequences.**

7_____Skipped Sequences   Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence:
    (OLD RULES)   (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
     (i)   SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
     (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
     This sequence is intentionally skipped

     Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to **include** the skipped sequences.

8_____Skipped Sequences   Sequence(s) _____ missing. If **intentional,** please insert the following lines for **each** skipped sequence.
    (NEW RULES)   <210> sequence id number
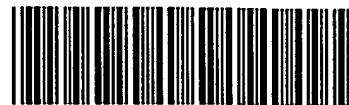   <400> sequence id number
     000

9_____Use of n's or Xaa's   Use of n's and/or Xaa's have been detected in the Sequence Listing.
    (NEW RULES)   Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
     In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.

10_____Invalid <213>   Per 1.823 of Sequence Rules, the only **valid** <213> responses are: Unknown, Artificial Sequence, or
    Response   scientific name (Genus/species). <220>-<223> section is **required** when <213> response is Unknown or
     is Artificial Sequence

11_____Use of <220>   Sequence(s) _____ missing the <220> "Feature" and associated numeric identifiers and responses.
     Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or
     "Unknown." Please explain source of genetic material in <220> to <223> section.
     (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)

12_____PatentIn 2.0   Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file,
    "bug"   resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence
     listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.

13_____Misuse of n/Xaa   "n" can only represent a single <u>nucleotide</u>; "Xaa" can only represent a single <u>amino acid</u>

IFWP

RAW SEQUENCE LISTING   DATE: 12/20/2005
PATENT APPLICATION: US/10/560,269   TIME: 11:19:31

          Input Set : A:\Sequence.ST25.txt
          Output Set: N:\CRF4\12202005\J560269.raw

      3 <110> APPLICANT: Segura, Dorotea Raventos
      4   Mygind, Per Holse
      5   Hogenhaug, Hans-Henrik Kristensen
      6   Tossi, Alessandro
      8 <120> TITLE OF INVENTION: Antimicrobial Peptides
     10 <130> FILE REFERENCE: 10496.204-US
C--> 12 <140> CURRENT APPLICATION NUMBER: US/10/560,269
C--> 12 <141> CURRENT FILING DATE: 2005-12-09
     12 <160> NUMBER OF SEQ ID NOS: 52
     14 <170> SOFTWARE: PatentIn version 3.3

Does Not Comply — Corrected Diskette Needed

ERRORED SEQUENCES

   1023 <210> SEQ ID NO: 52
   1024 <211> LENGTH: 19
   1025 <212> TYPE: DNA
   1026 <213> ORGANISM: Artificial
   1028 <220> FEATURE:
   1029 <223> OTHER INFORMATION: Primer 4 sequence
   1031 <400> SEQUENCE: 52
   1032 accgtagttg cgcccatcg   19
E--> 1038 (1 *delete*

(see p. 2 for more error)

pp 1-3

```
<220>
<221>  MISC_FEATURE
<222>  (18)..(18)
<223>  Xaa = Z or Z-arginine-tryptophane-leucine wherein Z =
       phenylalanine, leucine, arginine, alanine, glycine, valine,
       tyrosine, cysteine or proline

<400>  1

Gly Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
1               5                   10                  15

Xaa Xaa
```

OK, since it's explained

2

) variable length not permitted. see item 5 on Error Summary Sheet

Xaa cannot represent more than one amino acid

```
<210>  1
<211>  18
<212>  PRT
<213>  Artificial

<220>
<223>  Synthetic antimicrobial polypeptide

<220>
<221>  MISC_FEATURE
<222>  (2)..(2)
<223>  Xaa = leucine, isoleucine, tryptophane or methionine
```

tryptophan

```
<220>
<221>  MISC_FEATURE
<222>  (3)..(3)
<223>  Xaa = leucine, phenylalanine, tryptophane or valine
```

tryptophan

Input Set : **A:\Sequence.ST25.txt**
Output Set: **N:\CRF4\12202005\J560269.raw**

L:12 M:270 C: Current Application Number differs, Replaced Current Application No
L:12 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:124 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1 after pos.:0
L:128 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1 after pos.:16
L:1038 M:254 E: No. of Bases conflict, this line has no nucleotides.